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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:20:45 : Search time 5.40155 Seconds

(Without alignments)
798.574 Million cell updates/sec

Title: US-09-622-613B-11

Perfect score: 577
Sequence: 1 SDWLFFQKKHLTNTPRVDGN.....TFCVTCENQAPVHEVGVC 104

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SWISSProt.40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	551	95.5	104	RN30_RANPI
2	287	49.7	111	RNPO_RANCA
3	280.5	48.6	111	LECS_RANJA
4	264.5	45.8	111	RNPL_RANCA
5	144	25.0	119	RNP_IGUIG
6	132	22.6	124	RNP_GALMU
7	130.5	22.6	145	ANGR_MOUSE
8	130.5	22.6	146	ANGI_CERAE
9	128	22.2	148	ANGI_BOVIN
10	126	21.8	128	RNP_MYOCO
11	125	21.7	124	RNP_BALAC
12	121.5	21.1	146	ANGI_MACMU
13	120	20.8	128	RNP_CAVPO
14	120	20.8	128	RNP_PROGU
15	119.5	20.7	145	ANGI_MOUSE
16	118.5	20.5	146	ANGI_PAPPA
17	118	20.5	124	RNP_CHIBR
18	117	20.3	128	RNP_HYDHY
19	116	20.1	125	ANGI_RABIT
20	115	19.9	146	ANGI_MIOTA
21	114	19.8	124	RNP_HIPAM
22	113	19.6	147	ANGI_HUMAN
23	113	19.6	147	ANGI_PANTR
24	113	19.6	156	ECP3_MOUSE
25	112	19.4	124	RNP_PIG
26	112	19.4	128	RNP_HYSCR
27	112	19.4	150	RNP_BOVIN
28	112	19.4	156	RNP_MYOG
29	111.5	19.3	147	RNL4_HUMAN
30	111	19.2	128	RNP_HORSE
31	111	19.2	146	ANGI_SAISC
32	111	19.2	167	RNBR_BOVIN
33	110.5	19.2	123	ANGI_PIG

ALIGNMENTS

RESULT 1	34	110.5	19.2	155	1	ECP1_MOUSE	P97426	mus musculus
RN30_RANPI	35	110	19.1	124	1	RNPA_CAVPO	P00678	cavia porca
ID	36	110	19.1	141	1	RNBR_GIRCA	Q29542	giraffa cam
RN30_RANPI	37	110	19.1	146	1	ANGI_SAGOE	Q8W652	saquinus oe
STANDARD	38	110	19.1	151	1	RNBR_AXIPR	P87350	axis porcin
PRT: 104 AA.	39	110	19.1	156	1	ECP2_MOUSE	P97425	mus musculus
	40	109	18.9	123	1	ANG2_BOVIN	P80929	bos taurus
	41	109	18.9	124	1	RNP_AEPM	P07847	aepeyceros m
	42	109	18.9	124	1	RNP_ANTAM	P00668	antilocapra
	43	109	18.9	124	1	RNP_SHEEP	P00661	ovis aries
	44	108.5	18.8	150	1	RNK6_SAISC	Q46528	saimitri sci
	45	108.5	18.8	155	1	ECP_RAT	P70705	ratulus norv

AC	P22069:							
DT	01-AUG-1991 (Rel. 19, Created)							
DT	01-FEB-1994 (Rel. 20, Last sequence update)							
DT	01-FEB-1995 (Rel. 31, Last annotation update)							
DE	P-30 protein (EC 3.1.27.-) (Onconase).							
OS	Rana pipiens (Northern leopard frog).							
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.							
OX	NCB1_TaxID=8404;							
RA	[1]							
RP	SEQUENCE.							
RC	TISSUE=Embryo;							
RX	Medline=91093131; Pubmed=1985896;							
RA	Ardelt W., Mikulski S.M., Shogen K.;							
RT	"Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and early embryos. Homology to pancreatic ribonucleases.";							
RL	J. Biol. Chem. 266:245-251(1991).							
RM	[2]							
RP	3D-STRUCTURE MODELING.							
RX	Medline=93066156; Pubmed=1438177;							
RA	Mosmann S.C., Johns K.L., Ardelt W., Mikulski S.M., Shogen K.;							
RT	James M.N.G.;							
RT	"Comparative molecular modeling and crystallization of P-30 protein: a novel antitumor protein of Rana pipiens oocytes and early embryos.";							
RL	Proteins 14:392-400(1992).							
RN	[3]							
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).							
RX	Medline=94166079; Pubmed=8120892;							
RA	Mosmann S.C., Ardelt W., James M.N.G.;							
RT	"Refined 1.7 A x-ray crystallographic structure of P-30 protein, an amphibian ribonuclease with anti-tumor activity.";							
RL	J. Mol. Biol. 236:1141-1153(1994).							
CC	- FUNCTION: BASIC PROTEIN WITH ANTIPROLIFERATIVE/CYTOTOXIC ACTIVITY AGAINST SEVERAL TUMOR CELL LINES IN VITRO, AS WELL AS ANTITUMOR IN VIVO. IT EXHIBITS A RIBONUCLEASE-LIKE ACTIVITY AGAINST HIGH MOLECULAR WEIGHT RIBOSOMAL RNA.							
CC	- DEVELOPMENTAL STAGE: EARLY EMBRYOS (UP TO FOUR BLASTOMERE STAGE).							
CC	- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.							
DR	PDB: 1ONC; 31-JAN-94.							
DR	InterPro: IPR001427; RNaseA.							
DR	Pfam: PF00074; rnaase; 1.							
DR	Prodom: PD000535; RNaseA; 1.							
DR	SMART: SM00092; RNase_Pc; 1.							
DR	PROSITE: PS00127; RNASE_PANCREATIC; 1.							
KW	Hydrolase; Nuclease; Endonuclease; 3D-structure.							
FT	MOD_RES	1						
FT	ACT_SITE	10						
FT	ACT_SITE	31						
FT	ACT_SITE	97						
FT	DISULFID	19						
FT	DISULFID	30						
FT	DISULFID	48						
FT	DISULFID	90						

FT DISULFID 87 104
 FT HELIX 3 10
 FT STRAND 11 12
 FT HELIX 19 22
 FT TURN 23 24
 FT TURN 26 30
 FT STRAND 33 38
 FT HELIX 41 48
 FT TURN 49 50
 FT STRAND 55 58
 FT STRAND 63 70
 FT TURN 74 75
 FT STRAND 77 84
 FT STRAND 86 91
 FT TURN 92 93
 FT STRAND 94 101
 SO SEQUENCE 104 AA; 11845 MW; 22A753C2P9E56684 CRC64;

Query Match 95.5%; Score 551; DB 1; Length 104;
 Best Local Similarity 96.1%; Pred. No. 4.1e-52;
 Matches 99; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 DWLTFQKHLLTNTRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICGIIASKNVLTTS 61
 DB 2 DWLTFQKHLLTNTRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICGIIASKNVLTTS 61
 QY 62 EFTLSDCNVTSRPPCKYKLLKSTNFCVTCENQAPVHFVGVGHC 104
 DB 62 EFTLSDCNVTSRPPCKYKLLKSTNFCVTCENQAPVHFVGVGSC 104

RESULT 2

RNPO_RANCA STANDARD; PRT; 111 AA.
 AC P11916;

DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribonuclease, oocytes (EC 3.1.27.-) (RC-RNase) (Stallic acid-binding
 DE lectin) (SRI-C).
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_Taxid=8400;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Egg;
 RX MEDLINE=87299649; PubMed=3304421;
 RA Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,
 RT Takayanagi G., Hakomori S.;
 RT "Amino acid sequence of stallic acid binding lectin from frog (Rana
 RT catesbeiana) eggs";
 RL Biochemistry 26:2189-2194(1987).
 RN [2]
 RP CHARACTERIZATION, AND SEQUENCE OF 59-79.
 RX MEDLINE=92220613; PubMed=1373237;
 RA Liao Y.-D.;
 RT "A pyrimidine-guanine sequence-specific ribonuclease from Rana
 RT catesbeiana (bullfrog) oocytes";
 RL Nucleic Acids Res. 20:1371-1377(1992).
 RN [3]
 RP CHARACTERIZATION.

RC TISSUE=Egg;
 RX MEDLINE=93192604; PubMed=8448385;
 RA Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H.,
 RT Takayanagi Y., Hakomori S., Titani K.;
 RT "Ribonuclease activity of stallic acid-binding lectin from Rana
 RT catesbeiana eggs";
 RL Glycobiology 3:37-45(1993).
 RN [4]
 RP STRUCTURE BY NMR.
 RX MEDLINE=98437383; PubMed=9761686;
 RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T. H.;

"The solution structure of a cytotoxic ribonuclease from the oocytes
 of Rana catesbeiana (bullfrog).";
 J. Mol. Biol. 283:231-244(1998).
 CC -1- FUNCTION: PREFERENTIALLY CLEAVES SINGLE-STRANDED RNA AT PYRIMIDINE
 CC RESIDUES WITH A 3'FLANKING GUANINE. HYDROLYSES POLY(U) AND POLY(C)
 CC AS SUBSTRATES, AND PREFERENCES THE FORMER. THE S-LECTINS IN FROG EGGS
 CC MAY BE INVOLVED IN THE FERTILIZATION AND DEVELOPMENT OF THE FROG
 CC EMBRYO. THIS LECTIN AGGLOUTINATES VARIOUS ANIMAL CELLS, INCLUDING
 CC NORMAL LYMPHOCYTES, ERYTHROCYTES, AND FIBROBLASTS OF ANIMAL AND
 CC HUMAN ORIGIN.

CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR PIR: A27121; A27121.
 DR PDB: 1BC4; 28-OCT-98.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR ProSite: PS00127; RNASE_PANCREATIC; 1.
 KW Hydrolyase; Nuclease; Endonuclease; Stallic acid; Lectin; 3D-structure.
 FT MOD_RES 1 1
 FT ACT_SITE 10 10
 FT ACT_SITE 35 35
 FT ACT_SITE 103 103
 FT DISULFID 19 71
 FT DISULFID 34 81
 FT DISULFID 52 96
 FT DISULFID 93 110
 SO SEQUENCE 111 AA; 12464 MW; 0BC9E5F5729ECF4 CRC64;

Query Match 49.7%; Score 287; DB 1; Length 111;
 Best Local Similarity 49.1%; Pred. No. 6e-24;
 Matches 54; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

QY 2 DWLTFQKHLLTNTRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICGIIASKNV 57
 DB 2 DWLTFQKHLLTNTRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICGIIASKNV 57
 QY 58 LTTSEFTLSDCNVTSRPPCKYKLLKSTNFCVTCENQAPVHFVGVGHC 104
 DB 61 LSTTRQLNLTCTRTSTTPRCPYSSRTETNYICVNCENQAPVHFVGVGHC 110

RESULT 3

LECS_RANCA STANDARD; PRT; 111 AA.
 AC P18839;

DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Stallic acid-binding lectin (EC 3.1.27.-).
 OS Rana japonica (Japanese reddish frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_Taxid=8402;
 RN [1]
 RP SEQUENCE, AND DISULFIDE BONDS.

RC TISSUE=Egg;
 RX MEDLINE=91035319; PubMed=2229005;
 RA Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H.,
 RT Takayanagi Y., Titani K.;
 RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica)
 RT eggs";
 RL J. Biochem. 108:139-143(1990).
 CC -1- FUNCTION: THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE
 CC FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN
 CC PREFERENTIALLY AGGLOUTINATE A LARGE VARIETY OF TUMOR CELLS, BUT IT
 CC DOES NOT AGGLOUTINATE NON-TRANSFORMED CELLS AND ERYTHROCYTES.

CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR PIR: JX0120; JX0120.

Query Match	Similarity	45.8%	Score	264.5	DB 1	Length	111
Best Local	Similarity	42.7%	Pred. No.	1.5e-21			
Matches	47	Conservative	19	Mismatches	37	Indels	7
							Gaps
							2

Query	Match	Similarity	Score	DB 1	Length	Indels	Gaps
0Y	2	DMLTFKKHLNTRDVCNNIMSTNLF----	HCKDKNTFIYSRPEPKATCGIIASKNV	57			
DB	2	NMAAFKEKHIRSTSIDONTIMDKAITYVGCKERNFTFISSDDNKALICSSVSPRKE	61				
0Y	58	LTTSEFYISDC--NWTSPCKYKLLKSTNFTFCYTCENQAVHVGCHC	104				
DB	62	LSTTSFKLNTCIRDSITPRPCPRYPSPDNMKICVCKEOLPVHVEGICKC	111				

Query	Match	Similarity	Score	DB 1	Length	Indels	Gaps
0Y	2	DMLTFKKHLNTRDVCNNIMSTNLF----	HCKDKNTFIYSRPEPKATCGIIASKNV	57			
DB	2	NMAAFKEKHIRSTSIDONTIMDKAITYVGCKERNFTFISSDDNKALICSSVSPRKE	61				
0Y	51	ITASKNVLTJSE-FYLSDC--NWTSPCKYKLLKSTNFTFCYTCENQAVPHF	98				
DB	62	THYEDNLYDSNESFDLTDCKNVGGTAPSSCYNGTPTGKIRIRACENNQPVHF	114				

Query	Match	Similarity	Score	DB 1	Length	Indels	Gaps
0Y	2	DMLTFKKHLNTRDVCNNIMSTNLF----	HCKDKNTFIYSRPEPKATCGIIASKNV	57			
DB	2	NMAAFKEKHIRSTSIDONTIMDKAITYVGCKERNFTFISSDDNKALICSSVSPRKE	61				
0Y	51	ITASKNVLTJSE-FYLSDC--NWTSPCKYKLLKSTNFTFCYTCENQAVPHF	98				
DB	62	THYEDNLYDSNESFDLTDCKNVGGTAPSSCYNGTPTGKIRIRACENNQPVHF	114				

Query	Match	Similarity	Score	DB 1	Length	Indels	Gaps
0Y	2	DMLTFKKHLNTRDVCNNIMSTNLF----	HCKDKNTFIYSRPEPKATCGIIASKNV	57			
DB	2	NMAAFKEKHIRSTSIDONTIMDKAITYVGCKERNFTFISSDDNKALICSSVSPRKE	61				
0Y	51	ITASKNVLTJSE-FYLSDC--NWTSPCKYKLLKSTNFTFCYTCENQAVPHF	98				
DB	62	THYEDNLYDSNESFDLTDCKNVGGTAPSSCYNGTPTGKIRIRACENNQPVHF	114				

Query	Match	Similarity	Score	DB 1	Length	Indels	Gaps
0Y	2	DMLTFKKHLNTRDVCNNIMSTNLF----	HCKDKNTFIYSRPEPKATCGIIASKNV	57			
DB	2	NMAAFKEKHIRSTSIDONTIMDKAITYVGCKERNFTFISSDDNKALICSSVSPRKE	61				
0Y	51	ITASKNVLTJSE-FYLSDC--NWTSPCKYKLLKSTNFTFCYTCENQAVPHF	98				
DB	62	THYEDNLYDSNESFDLTDCKNVGGTAPSSCYNGTPTGKIRIRACENNQPVHF	114				

Query	Match	Similarity	Score	DB 1	Length	Indels	Gaps
0Y	2	DMLTFKKHLNTRDVCNNIMSTNLF----	HCKDKNTFIYSRPEPKATCGIIASKNV	57			
DB	2	NMAAFKEKHIRSTSIDONTIMDKAITYVGCKERNFTFISSDDNKALICSSVSPRKE	61				
0Y	51	ITASKNVLTJSE-FYLSDC--NWTSPCKYKLLKSTNFTFCYTCENQAVPHF	98				
DB	62	THYEDNLYDSNESFDLTDCKNVGGTAPSSCYNGTPTGKIRIRACENNQPVHF	114				

Query	Match	Similarity	Score	DB 1	Length	Indels	Gaps
0Y	2	DMLTFKKHLNTRDVCNNIMSTNLF----	HCKDKNTFIYSRPEPKATCGIIASKNV	57			
DB	2	NMAAFKEKHIRSTSIDONTIMDKAITYVGCKERNFTFISSDDNKALICSSVSPRKE	61				
0Y	51	ITASKNVLTJSE-FYLSDC--NWTSPCKYKLLKSTNFTFCYTCENQAVPHF	98				
DB	62	THYEDNLYDSNESFDLTDCKNVGGTAPSSCYNGTPTGKIRIRACENNQPVHF	114				

Query	Match	Similarity	Score	DB 1	Length	Indels	Gaps
0Y	2	DMLTFKKHLNTRDVCNNIMSTNLF----	HCKDKNTFIYSRPEPKATCGIIASKNV	57			
DB	2	NMAAFKEKHIRSTSIDONTIMDKAITYVGCKERNFTFISSDDNKALICSSVSPRKE	61				
0Y	51	ITASKNVLTJSE-FYLSDC--NWTSPCKYKLLKSTNFTFCYTCENQAVPHF	98				
DB	62	THYEDNLYDSNESFDLTDCKNVGGTAPSSCYNGTPTGKIRIRACENNQPVHF	114				

Query	Match	Similarity	Score	DB 1	Length	Indels	Gaps
0Y	2	DMLTFKKHLNTRDVCNNIMSTNLF----	HCKDKNTFIYSRPEPKATCGIIASKNV	57			
DB	2	NMAAFKEKHIRSTSIDONTIMDKAITYVGCKERNFTFISSDDNKALICSSVSPRKE	61				
0Y	51	ITASKNVLTJSE-FYLSDC--NWTSPCKYKLLKSTNFTFCYTCENQAVPHF	98	</			

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AC P00680;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN RNASE1 OR RN51.
OS Galesa musteloides (Culis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavillidae; Galea.
OX NCBI_TaxID=10146;
RN [1]
RP SEQUENCE
RX MEDLINE=87036770; PubMed=6571219;
RA Belintema J.J., Neuteboom B.;
RT "Origin of the duplicated ribonuclease gene in guinea-pig: comparison
RT of the amino acid sequences with those of two close relatives:
RT capybara and culis ribonuclease.";
RL J. Mol. Evol. 19:145-152(1983).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PANCREAS.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR PIR: A00827; NEUT.
DR HSSP: P00656; ISRN.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; rnasea; 1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Hydrolyase; Nuclease; Endonuclease.
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 41 41 BY SIMILARITY.
FT ACT_SITE 119 119 BY SIMILARITY.
FT VARIANT 1 1 MISSING (IN 1/3 OF THE MOLECULES).
SQ SEQUENCE 124 AA; 13870 MW; 609C7E251A7BBA25 CRC64;

Query Match 22.9%; Score 132; DB 1; Length 124;
Best Local Similarity 30.6%; Pred. No. 2.3e-07;
Matches 38; Conservative 18; Mismatches 36; Indels 32; Gaps 7;

OY 1 SDMLTFQKKHL-----TNRDVCNNIM---STNLFHCKDKNTFTISREPPYKATCKG 50
DB 3 SSAMKFORQHMDSGHPDTNTN--YCNEMVRSMTOGRCKRPVTFVHEPLEAVQAVC-- 58
OY 51 IIAKKNV-----LTTSEFYLDPCNVTSRP---CKYKLRKSTNTPFCVTGEN--QA 94
DB 59 --SOKNVPCKNGQNCYQSHSSMRTDCRYTSSSKYPNGCYTRMQAQKSIIVACEGTPSV 116
OY 95 PVHF 98
DB 117 PVHF 120

RESULT 7
ANGL_MOUSE STANDARD; PRT; 145 AA.
AC O64438;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Angiogenin-related protein precursor.
GN ANGRP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Liver;
RX MEDLINE=96079109; PubMed=8530072;
RA Brown W.E., Noble V., Subramanian V., Shapiro R.;
RT "The mouse angiogenin gene family: structures of an angiogenin-related
RT protein gene and two pseudogenes.";
RL Genomics 29:200-206(1995).
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: U22519; AAA91367.1; -.
DR HSSP: P03950; 1AAV.
DR MGP: MGI:104984; Angrp.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; rnasea; 1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Signal; Hydrolase; Nuclease; Endonuclease.
FT SIGNAL 1 24
FT CHAIN 25 145
FT MOD_RES 25 25
FT ACT_SITE 37 37 BY SIMILARITY.
FT ACT_SITE 64 64 BY SIMILARITY.
FT ACT_SITE 137 137 BY SIMILARITY.
FT DISULFID 50 104 BY SIMILARITY.
FT DISULFID 63 115 BY SIMILARITY.
FT DISULFID 81 130 BY SIMILARITY.
SQ SEQUENCE 145 AA; 16612 MW; 29A6EB814429C4AD CRC64;

Query Match 22.6%; Score 130.5; DB 1; Length 145;
Best Local Similarity 38.2%; Pred. No. 3.9e-07;
Matches 29; Conservative 11; Mismatches 29; Indels 7; Gaps 3;

OY 30 CKDNKTFYSREPPKATC--KGIASKNV-LTTSEFYLDPCNVTSR---PCKYKLRKS 82
DB 63 CKDVNTFHDHKKNNIKAKCGKSGSPYGRNLRISRFQVYTTCTYKGRSPRPCKYRASKG 122
OY 83 TNTECVTCENQAPVHF 98
DB 123 FRYIIIGCENGMPVHF 138

RESULT 8
ANGL_CERAE STANDARD; PRT; 146 AA.
AC O8WN66;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).
GN ANG OR RNASE5.
OS Cercopithecus aethiops (Green monkey) (Givete).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheinae; Cercopithecus;
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21918422; PubMed=11919285;
RA Zhang J., Rosenberg H.F.;
RT "Diversifying selection of the tumor-growth promoter angiogenin in
RT primate evolution.";

```

RL Mol. Biol. Evol. 19:438-445(2002).
 CC -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS
 CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS: ONCE BOUND,
 CC ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
 CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
 CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
 CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
 CC HYDROLYZING CELLULAR TRNAs (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 CC
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 CC
 CC EMBL: AF441661; AAL61646.1;
 CC Hydrolase; Nuclease; Endonuclease; Angiogenesis;
 CC Protein synthesis inhibitor; Signal
 CC SIGNAL 1 24
 CC CHAIN 25 146
 CC MOD_RES 25 25
 CC
 CC ACT_SITE 37 37 BY SIMILARITY.
 CC ACT_SITE 64 64 BY SIMILARITY.
 CC ACT_SITE 138 138 BY SIMILARITY.
 CC DISULFID 50 105 BY SIMILARITY.
 CC DISULFID 63 116 BY SIMILARITY.
 CC DISULFID 81 131 BY SIMILARITY.
 CC
 CC SEQUENCE 146 AA; 16444 MW; 27660112E85B8DF9 CRC64;
 SQ
 Query Match 22.6%; Score 130.5; DB 1; Length 146;
 Best Local Similarity 30.7%; Pred. No. 3.9e-07;
 Matches 31; Conservative 17; Mismatches 30; Indels 23; Gaps 4;
 Oy 5 TFOEHLNTRDVCNMINSTNLFCKDKDKNPTFYSRPEVKAIC--KGIASKNV-LNT 60
 Db 53 TMRNHLTSP-----CKDINTFIHGRHRIATICGDENGNPGENLRISK 97
 Oy 61 SEFYLSDCNMTS--TRCKYKYLKSTNFCVTCENQAPVH 97
 Db 98 SPFYVTCTNLKRGSPRRCQYRATGSRNIVYGCNGLPVH 138
 RESULT 9
 ANGI_BOVIN STANDARD: PRT: 148 AA;
 ID ANGI_BOVIN STANDARD: PRT: 148 AA;
 AC P10152; O9GK99;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Angiogenin-1 precursor (EC 3.1.27.-).
 GN ANGI OR ANG.
 OS Bos taurus (Bovidae).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 CC NCB1_TaxID=5913;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Chang S.-I.;
 RT "Cloning, sequencing, and expression of bovine angiogenin."
 RL Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 24-148.
 RC TISSUE=Milk;
 RX MEDLINE=89055101; PubMed=3197838;
 RA Maes P., Damart D., Rommens C., Montreuil J., Spik G., Tartar A.;
 RT "The complete amino acid sequence of bovine milk angiogenin."

RL FEBS Lett. 241:41-45(1988).
 RN [3]
 RP SEQUENCE OF 24-148.
 RC TISSUE=Plasma;
 RX MEDLINE=89375344; PubMed=2775757;
 RA Bond M.D., Strydom D.J.;
 RT "Amino acid sequence of bovine angiogenin."
 RL Biochemistry 28:6110-6113(1989).
 RN [4]
 RP CHARACTERIZATION, AND SEQUENCE OF 25-55.
 RC TISSUE=Plasma;
 RX MEDLINE=89118214; PubMed=3064806;
 RA Bond M.D., Vallee B.L.;
 RT "Isolation of bovine angiogenin using a placental ribonuclease
 RT inhibitor binding assay."
 RL Biochemistry 27:6282-6287(1988).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
 RX MEDLINE=95224057; PubMed=7708754;
 RA Acharya K.R., Shaprio R., Riordan J.F., Vallee B.L.;
 RT "Crystal structure of bovine angiogenin at 1.5-A resolution."
 RL Proc. Natl. Acad. Sci. U.S.A. 92:2949-2953(1995).
 RN [6]
 RP STRUCTURE BY NMR.
 RX MEDLINE=96280645; PubMed=8688423;
 RA Leguin O., Albaret C., Bontems F., Spik G., Lallemand J.-Y.;
 RT "Solution structure of bovine angiogenin by 1H nuclear magnetic
 RT resonance spectroscopy."
 RL Biochemistry 35:8670-8680(1996).
 CC -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS
 CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS: ONCE BOUND,
 CC ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
 CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
 CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
 CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
 CC HYDROLYZING CELLULAR TRNAs. BINDS TIGHTLY TO PLACENTAL
 CC RIBONUCLEASE INHIBITOR AND HAS VERY LOW RIBONUCLEASE ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: SERUM, AND MILK.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AF135124; AAC47631.1;
 CC PIR: A32474; A32474.
 CC PDB: 1AG1; 03-APR-96.
 CC PDB: 1G10; 07-DEC-96.
 CC InterPro: IPR001427; RNaseA.
 CC Pfam: PF00074; RNaseA; 1.
 CC PRINTS: PR00794; RIBONUCLEASE.
 CC PRODOM: PD000535; RNaseA; 1.
 CC SMART: SM00092; RNase_Pc; 1.
 CC PROSITE: PS00127; RNASE_PANCREATIC; 1.
 CC Hydrolase; Nuclease; Endonuclease; Angiogenesis;
 CC Protein synthesis inhibitor; Signal; 3D-structure.
 CC SIGNAL 1 23
 CC CHAIN 24 148
 CC ACT_SITE 37 37 ANGIOGENIN-1.
 CC ACT_SITE 64 64
 CC ACT_SITE 138 138
 CC DISULFID 50 105
 CC DISULFID 63 116
 CC DISULFID 81 131
 CC
 CC SEQUENCE 148 AA; 16969 MW; B7999124CB8523DD CRC64;
 SQ
 Query Match 22.2%; Score 128; DB 1; Length 148;
 Best Local Similarity 34.0%; Pred. No. 7.3e-07;

Matches 33; Conservative 14; Mismatches 32; Indels 18; Gaps 5;

OY 16 DVDCCNNIMSTNLF--HCKDKNTFIYSRPEVKAICKGIISKV-----VLTSEFY 65
 47 DECFPMKMRKRLTRCKDKDNTITHGKNDIKAIICE-----DRNGQPRGLRISKSEFOT 102
 Db 66 SDC---NVTSR-PCKYKLLKSTNTPCVTCENQAPVHF 98
 103 TICKHKGSSRPPCRGATEDSRIVYVGCENGLPVHF 139

RESULT 10

RNP_MYOCO STANDARD; PRT; 128 AA.
 ID RNP_MYOCO
 AC P00676;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
 GN RNASE1 OR RNS1.
 OS Myocastor coypus (Coypu) (Nutria).
 OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Myocastoridae;
 OC Myocastor.
 OC NCBI_TaxID=10157;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pancreas;
 RX MEDLINE=7065676; PubMed=999896;
 RA van den Berg A., van den Hende-Timmer L., Beintema J.J.;
 RT Isolation, properties and primary structure of coypu and chinchilla
 RL pancreatic ribonuclease.";
 RL Biochim. Biophys. Acta 453:400-409(1976).
 CC -1 CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
 with 2',3'-cyclic phosphate intermediates.
 CC -1 SUBCELLULAR LOCATION: Secreted.
 CC -1 TISSUE SPECIFICITY: PANCREAS.
 CC -1 SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR PIR: A00822; NRCU.
 DR HSSP: P00656; ISRN.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA.1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR ProDom: PD000535; RNaseA.1.
 DR SMART: SM00092; RNase_Pc.1.
 DR PROSITE: PS00127; RNASE_PANCREATIC.1.
 DR KMW: K00001; RNaseA.1.
 FT DISULFID 26 84
 FT DISULFID 40 95
 FT DISULFID 58 110
 FT DISULFID 65 72
 FT ACT_SITE 12 12
 FT ACT_SITE 41 41
 FT ACT_SITE 119 119
 FT CARBOHYD 34 34
 SO SEQUENCE 128 AA; 14267 MW; 4EB924E52B445832 CRC64;

Query Match 21.8%; Score 126; DB 1; Length 128;

Best Local Similarity 29.9%; Pred. No. 1e-06; Mismatches 36; Indels 28; Gaps 7;

OY 6 FOKKHL-----TNTRDVDCNNIM-STNLF--HCKDKNTFIYSRPEVKAICKGIISKV 57
 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
 GN RNASE1 OR RNS1.
 OS Myocastor coypus (Coypu) (Nutria).
 OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Myocastoridae;
 OC Myocastor.
 OC NCBI_TaxID=10157;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pancreas;
 RX MEDLINE=7065676; PubMed=999896;
 RA van den Berg A., van den Hende-Timmer L., Beintema J.J.;
 RT Isolation, properties and primary structure of coypu and chinchilla
 RL pancreatic ribonuclease.";
 RL Biochim. Biophys. Acta 453:400-409(1976).
 CC -1 CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
 with 2',3'-cyclic phosphate intermediates.
 CC -1 SUBCELLULAR LOCATION: Secreted.
 CC -1 TISSUE SPECIFICITY: PANCREAS.
 CC -1 SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR PIR: A00822; NRCU.
 DR HSSP: P00656; ISRN.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA.1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR ProDom: PD000535; RNaseA.1.
 DR SMART: SM00092; RNase_Pc.1.
 DR PROSITE: PS00127; RNASE_PANCREATIC.1.
 DR KMW: K00001; RNaseA.1.
 FT DISULFID 26 84
 FT DISULFID 40 95
 FT DISULFID 58 110
 FT DISULFID 65 72
 FT ACT_SITE 12 12
 FT ACT_SITE 41 41
 FT ACT_SITE 119 119
 FT CARBOHYD 34 34
 SO SEQUENCE 128 AA; 14267 MW; 4EB924E52B445832 CRC64;

RESULT 11

RNP_BALAC

ID RNP_BALAC STANDARD; PRT; 124 AA.

AC P00673;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
 GN RNASE1 OR RNS1.
 OS Balaenoptera acutorostrata (Minke whale) (Lesser rorqual).
 OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
 OC Balaenopteridae; Balaenoptera.
 OC NCBI_TaxID=9767;
 RN [1]
 RP SEQUENCE.
 RC MEDLINE=7627855; PubMed=962870;
 RA Emmens M., Welling G.W., Beintema J.J.;
 RT "The amino acid sequence of pike-whale (lesser-rorqual) pancreatic
 RL ribonuclease.";
 RL Biochem. J. 157:317-323(1976).
 CC -1 CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
 with 2',3'-cyclic phosphate intermediates.
 CC -1 SUBCELLULAR LOCATION: Secreted.
 CC -1 TISSUE SPECIFICITY: PANCREAS.
 CC -1 SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR PIR: A00818; NRMK.
 DR HSSP: P00656; ISRN.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA.1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR ProDom: PD000535; RNaseA.1.
 DR SMART: SM00092; RNase_Pc.1.
 DR PROSITE: PS00127; RNASE_PANCREATIC.1.
 DR KMW: K00001; RNaseA.1.
 FT DISULFID 26 84
 FT DISULFID 40 95
 FT DISULFID 58 110
 FT DISULFID 65 72
 FT ACT_SITE 12 12
 FT ACT_SITE 41 41
 FT ACT_SITE 119 119
 FT CARBOHYD 76 76
 SO SEQUENCE 124 AA; 14125 MW; F57475459F697820 CRC64;

Query Match 21.7%; Score 125; DB 1; Length 124;

Best Local Similarity 28.6%; Pred. No. 1.3e-06; Mismatches 42; Indels 28; Gaps 6;

Matches 34; Conservative 15; Mismatches 42; Indels 28; Gaps 6;

OY 4 LPEOKKHLTNTRDVD-----CNNIMSTNLF--HCKDKNTFIYSRPEVKAICKGIISKV 55
 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
 GN RNASE1 OR RNS1.
 OS Myocastor coypus (Coypu) (Nutria).
 OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Myocastoridae;
 OC Myocastor.
 OC NCBI_TaxID=10157;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pancreas;
 RX MEDLINE=7065676; PubMed=999896;
 RA van den Berg A., van den Hende-Timmer L., Beintema J.J.;
 RT Isolation, properties and primary structure of coypu and chinchilla
 RL pancreatic ribonuclease.";
 RL Biochim. Biophys. Acta 453:400-409(1976).
 CC -1 CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
 with 2',3'-cyclic phosphate intermediates.
 CC -1 SUBCELLULAR LOCATION: Secreted.
 CC -1 TISSUE SPECIFICITY: PANCREAS.
 CC -1 SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR PIR: A00822; NRCU.
 DR HSSP: P00656; ISRN.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA.1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR ProDom: PD000535; RNaseA.1.
 DR SMART: SM00092; RNase_Pc.1.
 DR PROSITE: PS00127; RNASE_PANCREATIC.1.
 DR KMW: K00001; RNaseA.1.
 FT DISULFID 26 84
 FT DISULFID 40 95
 FT DISULFID 58 110
 FT DISULFID 65 72
 FT ACT_SITE 12 12
 FT ACT_SITE 41 41
 FT ACT_SITE 119 119
 FT CARBOHYD 76 76
 SO SEQUENCE 124 AA; 14125 MW; F57475459F697820 CRC64;

Query Match 21.7%; Score 125; DB 1; Length 124;

Best Local Similarity 28.6%; Pred. No. 1.3e-06; Mismatches 42; Indels 28; Gaps 6;

OY 6 FOKKHLTNTRDVD-----CNNIMSTNLF--HCKDKNTFIYSRPEVKAICKGIISKV 55
 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
 GN RNASE1 OR RNS1.
 OS Myocastor coypus (Coypu) (Nutria).
 OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Myocastoridae;
 OC Myocastor.
 OC NCBI_TaxID=10157;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pancreas;
 RX MEDLINE=7065676; PubMed=999896;
 RA van den Berg A., van den Hende-Timmer L., Beintema J.J.;
 RT Isolation, properties and primary structure of coypu and chinchilla
 RL pancreatic ribonuclease.";
 RL Biochim. Biophys. Acta 453:400-409(1976).
 CC -1 CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
 with 2',3'-cyclic phosphate intermediates.
 CC -1 SUBCELLULAR LOCATION: Secreted.
 CC -1 TISSUE SPECIFICITY: PANCREAS.
 CC -1 SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR PIR: A00822; NRCU.
 DR HSSP: P00656; ISRN.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA.1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR ProDom: PD000535; RNaseA.1.
 DR SMART: SM00092; RNase_Pc.1.
 DR PROSITE: PS00127; RNASE_PANCREATIC.1.
 DR KMW: K00001; RNaseA.1.
 FT DISULFID 26 84
 FT DISULFID 40 95
 FT DISULFID 58 110
 FT DISULFID 65 72
 FT ACT_SITE 12 12
 FT ACT_SITE 41 41
 FT ACT_SITE 119 119
 FT CARBOHYD 76 76
 SO SEQUENCE 124 AA; 14125 MW; F57475459F697820 CRC64;

RESULT 12

ANGI_MACMU

ANGI_MACMU

STANDARD; PRT; 146 AA.

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).

GN ANG OR RNASE5.

OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecinae; Macaca.

OC NCBI_TaxID=9544;

OX [1]

RP SEQUENCE FROM N.A.
 RA MEDLINE=21918422; PubMed=11919285;
 RT "diversifying selection of the tumor-growth promoter angiogenin in
 RT primate evolution.";
 RL Mol. Biol. Evol. 19:438-445(2002).
 CC -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS
 CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,
 CC ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
 CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
 CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
 CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
 CC HYDROLYZING CELLULAR TRNAs (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF41657; AAL6149.1;
 KM Hydrolyase; Nuclease; Endonuclease; Angiogenesis;
 KW Protein synthesis inhibitor; Signal.
 FT SIGNAL 1 24
 FT CHAIN 1 146
 FT MOD_RRS 25 146
 FT 25 146
 FT ACT_SITE 37 37
 FT ACT_SITE 64 64
 FT ACT_SITE 138 138
 FT DISULFID 50 105
 FT DISULFID 63 116
 FT DISULFID 81 131
 SQ SEQUENCE 146 AA; 16301 MW; E39A89215DB2A2A4 CRC64;
 Query Match 21.1%; Score 121.5; DB 1; Length 146;
 Best Local Similarity 28.7%; Pred. No. 3.5e-06;
 Matches 29; Conservative 17; Mismatches 32; Indels 23; Gaps 4;
 QY 5 TPQKHLLTNRDVCNNIMSTNLFHCKDKNTFYISRPEPKAIC---KGIISKNV-LPT 60
 Db 53 TMRRLHLPSP-----CKDITFVHGNNHHHTALICDGDNGSPYGNLAKIST 97
 QY 61 SEFYLSDCNVTST---RPEKYKLLKSTNTPFCVTCENQAPVH 97
 Db 98 SFFQVTFCKLRGSGSPRPPCOYRATRGSRNIVGCEGLPYH 138
 RESULT 13
 RNP_CAVPO STANDARD; PRT; 128 AA.
 ID RNP_CAVPO
 AC P00679;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribonuclease pancreatic B (EC 3.1.27.5) (Rnase 1B).
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pancreas;
 RX MEDLINE=77185023; PubMed=862624;
 RA van den Berg A., van den Hende-Timmer L., Hofsteenge J., Gastra W.,
 RA Beutema J.J.;
 RT "Guinea-pig pancreatic ribonucleases. Isolation, properties, primary
 RT structure and glycosylation."
 RL Eur. J. Biochem. 75:91-100(1977).

CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
 CC with 2',3'-cyclic phosphate intermediates.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: PANCREAS.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 CC -----
 DR PIR; A00826; NRGPB.
 DR HSSP; P00656; ISRN.
 DR InterPro: IPR001427; RnaseA.
 DR Pfam: PF00074; RnaseA.1.
 DR PRINTS; PR00794; RIBONUCLEASE.
 DR ProDom: PD000535; RnaseA; 1.
 DR SMART; SM00092; Rnase_Pc; 1.
 DR PROSITE; PS00127; Rnase_PANCREATIC; 1.
 KW Hydrolyase; Nuclease; Endonuclease; glycoprotein.
 FT DISULFID 26 84
 FT DISULFID 40 95
 FT DISULFID 58 110
 FT DISULFID 65 72
 FT ACT_SITE 12 12
 FT ACT_SITE 12 12
 FT ACT_SITE 41 41
 FT ACT_SITE 119 119
 FT CARBOHYD 21 21
 FT CARBOHYD 34 34
 FT VARIANT 64 64
 FT VARIANT L->P.
 SQ SEQUENCE 128 AA; 14406 MW; A2F4101A1A33E93B CRC64;
 Query Match 20.8%; Score 120; DB 1; Length 128;
 Best Local Similarity 28.3%; Pred. No. 4.4e-06;
 Matches 35; Conservative 21; Mismatches 37; Indels 30; Gaps 7;
 QY 1 SDMTTFQKHLLTNRDVCNNIM---STNLFHCKDKNTFYISRPEPKAICGKI 51
 Db 3 SSAMKFPQRLMDPBGSSNSNT-CNVMMIRNNITQRCRFVNTFVIESLADQAVC--- 58
 QY 52 IASKNVLT-----TSEFYLSDCNVTST---RPEKYKLLKSTNTPFCVTCENQ-AP 95
 Db 59 -FQKNVLCKNGQNTCYGYSRMRITDCRVTSKFPNCYSRMSQAKSIVACEGDYRYP 117
 QY 96 VHF 98
 Db 118 VHF 120
 RESULT 14
 RNP_PROGU STANDARD; PRT; 128 AA.
 ID RNP_PROGU
 AC P04059;
 DT 01-NOV-1986 (Rel. 03, Created)
 DT 01-NOV-1986 (Rel. 03, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribonuclease pancreatic (EC 3.1.27.5) (Rnase 1) (Rnase A).
 GN RNAS1 OR RN1.
 OS Proechimys guairae (Castiagua).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Echymidae; Proechimys.
 OX NCBI_TaxID=10163;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pancreas;
 RX MEDLINE=83000399; PubMed=7115727;
 RA Beutema J.J., Knol G., Martena B.;
 RT "The primary structures of pancreatic ribonucleases from African
 RT porcupine and castiagua, two hystriocormorph rodent species."
 RL Biochim. Biophys. Acta 705:102-110(1982).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
 CC with 2',3'-cyclic phosphate intermediates.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: PANCREAS.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR PIR; A00821; NRKS.
 DR HSSP; P00656; ISRN.

DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR Prodom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNaseA; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
 KW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.
 FT DISULFID 26 84 BY SIMILARITY.
 FT DISULFID 40 95 BY SIMILARITY.
 FT DISULFID 58 110 BY SIMILARITY.
 FT DISULFID 65 112 BY SIMILARITY.
 FT ACT_SITE 12 12 BY SIMILARITY.
 FT ACT_SITE 41 41 BY SIMILARITY.
 FT ACT_SITE 119 119 BY SIMILARITY.
 FT CARBOHYD 34 34 N-LINKED (GLCNAC...)
 SQ SEQUENCE 128 AA: 14244 MW: 2DBS8093A9D3C936 CRC64;
 Query Match 20.8%; Score 120; DB 1; Length 128;
 Best Local Similarity 29.9%; Pred. No. 4; 4e-06;
 Matches 35; Conservative 18; Mismatches 36; Indels 28; Gaps 7;
 QY 6 FOKKHL-----TTRVDCCNINM-STNLF--HCKDKNTFYSPREPVKAIKGIASKNV 57
 DB 8 FOKHIDSSGSPSTNPVNCNAMKSRNMQERCKPVTFVHEPLADVAVC-----FOKNV 63
 QY 58 -----LTFSEFYLSDCNVTSR---PCKYKLLKSTNFCVYCENQ--APVHF 98
 DB 64 PCKNGSNCYEISNMHITDCRLTNSKFPDCLVTRTSEKSLTVACENPPVPHF 120
 RESULT 15
 ANGI_MOUSE STANDARD: PRT: 145 AA.
 ID ANGI_MOUSE P21570:
 AC 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Angiogenin precursor (EC 3.1.27.-).
 GN ANG.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91025023; PubMed=2222458;
 RA Bond M.D., Vallee B.L.;
 RT "Isolation and sequencing of mouse angiogenin DNA";
 RL Biochem. Biophys. Res. Commun. 171:988-995(1990).
 RN [2]
 RP PARTIAL SEQUENCE.
 RC TISSUE-Serum;
 RX MEDLINE=93192291; PubMed=8448182;
 RA Bond M.D., Strzydom D.J., Vallee B.L.;
 RT "Characterization and sequencing of rabbit, pig and mouse
 RT angiogenins: discernment of functionally important residues and
 RT regions";
 RL Biochim. Biophys. Acta 1162:177-186(1993).
 CC -!- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS
 CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,
 CC ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
 CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
 CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
 CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
 CC HYDROLYZING CELLULAR TRNAs.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: U22516; AAA91366.1; -.
 DR PIR: A35932; A35932.
 DR HSSP: P03950; 1A4Y.
 DR MGD: MGI:88022; Ang.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR Prodom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNaseA; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
 KW Hydrolyase; Nuclease; Endonuclease; Angiogenesis;
 KW Protein synthesis inhibitor; Signal.
 FT CHAIN 1 24
 FT SIGNAL 1 24
 FT MOD_RES 25 25
 FT ACT_SITE 37 37 BY SIMILARITY.
 FT ACT_SITE 64 64 BY SIMILARITY.
 FT ACT_SITE 137 137 BY SIMILARITY.
 FT DISULFID 50 104 BY SIMILARITY.
 FT DISULFID 63 115 BY SIMILARITY.
 FT DISULFID 81 130 BY SIMILARITY.
 SQ SEQUENCE 145 AA: 16228 MW: 06944260B8764938 CRC64;
 Query Match 20.7%; Score 119.5; DB 1; Length 145;
 Best Local Similarity 30.8%; Pred. No. 5; 7e-06;
 Matches 33; Conservative 12; Mismatches 45; Indels 17; Gaps 5;
 QY 9 KHLTNRDVID-----CNIMSTNLF--HCKDKNTFYSPREPVKAIKGIASKNV 56
 DB 32 KFLQHHDAKPKGRDORCERMKRSLSPCKDVNTFTHGKSNIKAIKGNAGSPYREN 91
 QY 57 V-LTFSEFYLSDCNVTSR---PCKYKLLKSTNFCVYCENQAPVHF 98
 DB 92 LKMSKSPFQVTVCKHTGSGSPRPPCOYRASAGFRHVIVACENGLPVHF 138

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 Job time : 6.40155 secs